Göbl, Morris & Van Dam et al. Fig S9

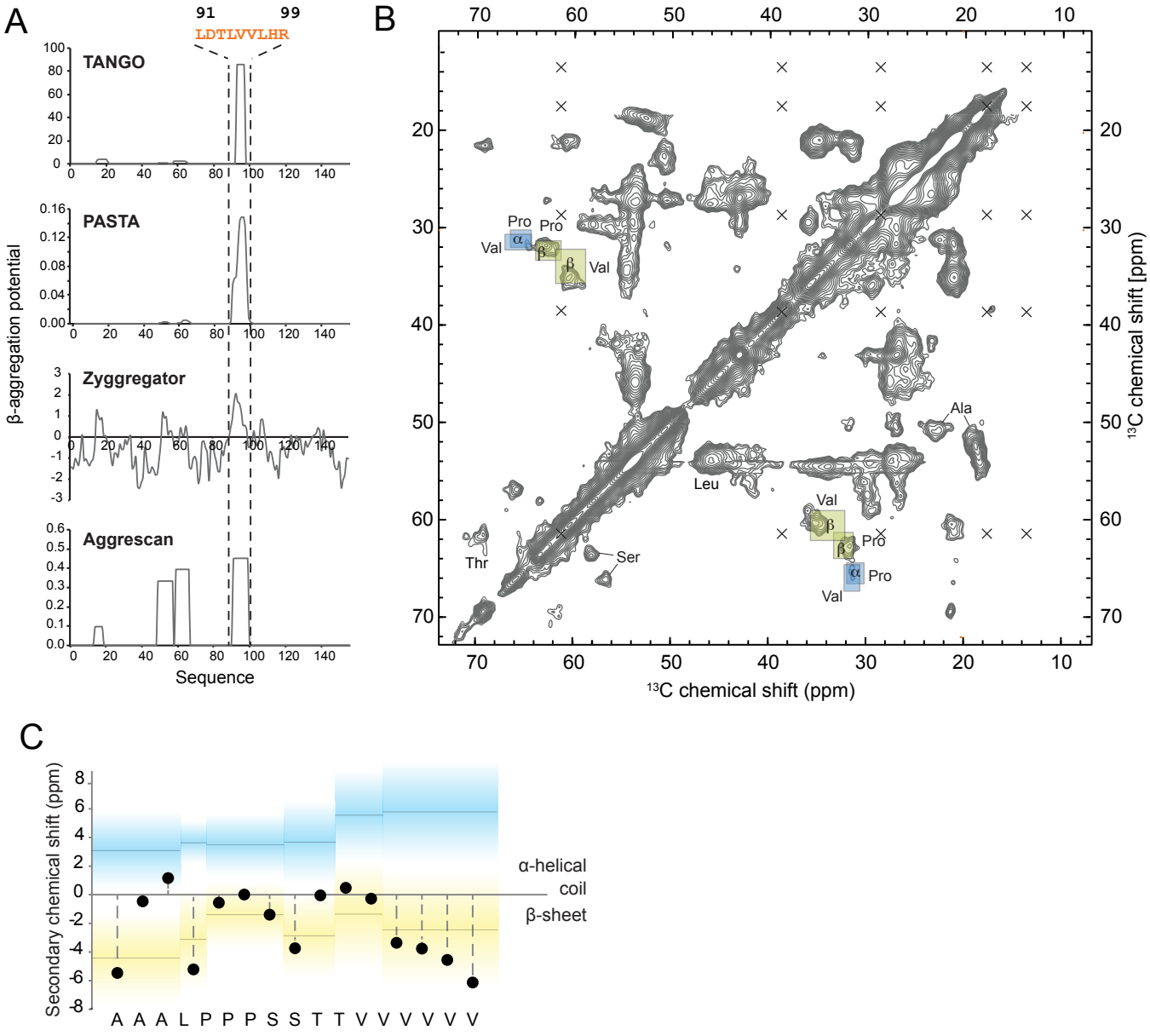

Figure S9. Prediction of p16INK4A aggregation-prone regions
(A) Four β-aggregation prediction algorithms predict that residues 90 to 99 of p16^{INK4A} have high aggregation propensity. **(B)** $^{13}C^{13}C$ solid state NMR spectrum of p16^{INK4A} fibrils showing the full aliphatic region. Crosses mark positions where peaks would be expected to arise from isoleucine residues. There are three isoleucines in the full p16^{INK4A} sequence, suggesting that these residues are absent from the folded β-sheet core of p16^{INK4A} fibrils. Peaks that correspond to amino acid types with distinct shifts are labelled. Boxes indicate the average shift expected for both secondary-structure types of proline and valine, within one standard deviation.
(C) ^{13}C Secondary chemical shifts of uniquely assigned amino acid types showing the presence of β-sheet secondary structural elements. Horizontal lines indicate average values for secondary chemical shifts of alpha-helix (blue) and β-sheet (yellow), and regions are shaded to one standard deviation.